



23 **Abstract**

24 Interferon lambda 4 (*IFNL4*) is a recently identified enigmatic member of the  
25 interferon lambda family. Genetic data suggest that the *IFNL4* gene acts in a pro-viral  
26 and anti-inflammatory manner in patients. However, the protein is *in vitro*  
27 indistinguishable from the other members of the interferon lambda family. We have  
28 investigated the gene regulation of *IFNL4* in detail and found that it differs radically  
29 from that of canonical antiviral interferons. Being induced by viral infection is a  
30 defining characteristic of interferons, but viral infection or overexpression of  
31 members of the interferon regulatory factor (IRF) family of transcription factors only  
32 leads to a minute induction of *IFNL4*. This behavior is evolutionarily conserved and  
33 can be reversed by inserting a functional IRF3 binding site into the *IFNL4* promoter.  
34 Thus, the regulation of the *IFNL4* gene is radically different and might explain some  
35 of the atypical phenotypes associated with the *IFNL4* gene in humans.

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45 **Importance**

46 Recent genetic evidence has highlighted how the *IFNL4* gene acts in a  
47 counterintuitive manner as patients with a non-functional *IFNL4* gene exhibit  
48 increased clearance of hepatitis C virus but also increased liver inflammation. This  
49 suggests that the *IFNL4* gene acts in a pro-viral and anti-inflammatory manner. Those  
50 surprising but quite clear genetic data have prompted an extensive examination of the  
51 basic characteristics of the *IFNL4* gene and its gene product IFN- $\lambda$ 4. We have  
52 investigated the expression of the *IFNL4* gene and found it to be poorly induced by  
53 viral infections. A thorough investigation of the *IFNL4* promoter revealed a highly  
54 conserved and functional promoter, but also one that lacks the defining characteristic  
55 of IFNs, i.e. the ability to be effectively induced by viral infections. We suggest that  
56 the unique function of the *IFNL4* gene is related to its non-canonical transcriptional  
57 regulation.

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68 **Introduction**

69 Interferons (IFNs) are divided into three families according to their distinct receptor  
70 utilization: type I (e.g. IFN- $\alpha/\beta$ ), type II (IFN- $\gamma$ ) and type III (IFN- $\lambda$ ). Both type I and  
71 type III IFNs are potent antiviral cytokines (1). Type II IFN also possesses some  
72 antiviral effect but its primary function is to link the innate and adaptive parts of the  
73 immune system (2). Type I and type III IFNs play a key role in innate immunity  
74 towards viral infection and their expression is induced by viral infection in both  
75 immune and non-immune cells (3-5). Humans possess four type III IFN genes known  
76 as *IFNL1*, *IFNL2*, *IFNL3* and *IFNL4*. *IFNL1-3* share a high degree of similarity and  
77 were identified as a novel family of genes encoding virally induced IFNs by two  
78 independent teams in 2003 (6, 7). In the following decade, genome-wide association  
79 studies linked clearance of hepatitis C virus (HCV) to genetic variation within the  
80 type III IFN loci (8-11), and this subsequently led to the discovery of the *IFNL4* gene  
81 when genetic data was compared with RNA-sequencing analysis (12). The DNA  
82 sequence similarity between the *IFNL4* gene and the *IFNL1-3* genes is relative low  
83 and at the protein level the identity is approximately 28% (13). The *IFNL4* gene is  
84 well conserved among mammals, except in rodents where the gene is absent.

85 Upon identification of the *IFNL4* gene, the authors also identified a dinucleotide  
86 variant ( $\Delta G/TT$ , rs368234815) situated in the first exon of the *IFNL4* gene (12). The  
87 *IFNL4*-TT frameshift mutation was introduced during early human evolution, before  
88 the “out of Africa” scenario (14). There has subsequently been a positive selection for  
89 the *IFNL4*-TT allele resulting in this being the major allele in humans, but with major  
90 variations in allele frequency between different human populations. The  $\Delta G/TT$   
91 variation is associated with the rate of spontaneous HCV clearance as well as the

92 response to treatment (12). The *IFNL4*-ΔG is the ancestral allele and generates the  
93 full-length IFN-λ4 protein, whereas the *IFNL4*-TT allele leads to a frameshift and  
94 therefore aborted expression of IFN-λ4. Surprisingly, patients harboring the  
95 functional *IFNL4*-ΔG allele have a lower HCV clearance rate compared to those  
96 patients, who have the *IFNL4*-TT allele (12). Interestingly, the *IFNL4*-ΔG allele is  
97 also associated with lower liver inflammation and fibrosis in HCV-infected patients  
98 (15-17) as well as patients with non-alcoholic fatty liver disease (18, 19). Thus, the  
99 genetic evidence suggests that *in vivo*, the *IFNL4* gene acts in a pro-viral and anti-  
100 inflammatory manner, quite in contrast to the pro-inflammatory and anti-viral effect  
101 of other type III IFNs. Here, we will use the term canonical IFNs about all type I and  
102 type III IFN genes, except *IFNL4*.

103 Biochemically, the IFN-λ4 protein acts in a manner similar to the proteins encoded by  
104 the canonical type III IFN genes. It signals through the canonical IFN-λ receptor  
105 complex (20) and induces a set of genes highly similar to that induced by the  
106 canonical members of the IFN-λ family (20, 21). Despite its clear antiviral activity *in*  
107 *vitro*, the causal role of the IFN-λ4 protein in lower HCV clearance rates is supported  
108 by the finding that a single amino acid substitution of a proline to a serine at position  
109 70 (IFN-λ4 P70S) in IFN-λ4 substantially affects the antiviral activity of the protein  
110 (22). HCV patients harboring the impaired IFN-λ4 S70 variant display lower IFN-  
111 stimulated gene (ISG) expression levels but better treatment response rates and better  
112 spontaneous clearance rates, when compared to patients coding for the fully active  
113 IFN-λ4 P70 variant (22). Finally, comprehensive genome-to-genome analysis in  
114 chronically infected HCV patients supported a role for the *IFNL4* gene as the  
115 causative gene. In this study, *IFNL4* genotype determined viral load and affected the  
116 evolution of HCV quasispecies within patients (23). Thus, the result is a paradox

117 where the IFN- $\lambda$ 4 protein is antiviral *in vitro* but appears to be “pro-viral” and “anti-  
118 inflammatory” *in vivo*.

119 Several attempts have been made to measure induction of the *IFNL4* gene during viral  
120 infection, both *in vivo* and *in vitro*. Expression of *IFNL4* mRNA was not detected in  
121 peripheral blood mononuclear cells from chronically infected HCV patients (24).  
122 Similarly, several other studies measured either no or very low *IFNL4* mRNA  
123 expression in liver samples from patients with either non-viral liver diseases, chronic  
124 hepatitis B virus infection or chronic HCV infection (25-27). Finally, both stimulation  
125 with pathogen-associated molecular patterns (PAMP) and viral infection of different  
126 hepatoma cell lines or primary human hepatocytes resulted in minimal expression of  
127 *IFNL4* but strong expression of the canonical *IFNL3* (28). Together these  
128 observations led to speculation that the *IFNL4* promoter is non-functional and that this  
129 is part of a general trend during human evolution to abrogate expression of the IFN- $\lambda$ 4  
130 protein.

131 It is currently unclear why the IFN- $\lambda$ 4 protein became a liability in humans, whereas  
132 it is retained in most other mammalian species. To explain the unique genetic  
133 observations linked to the *IFNL4* gene, we searched for characteristics of the *IFNL4*  
134 gene that differentiates it from the canonical IFNs. Here, we demonstrate that the  
135 *IFNL4* promoter is indeed functional and that the mode of gene regulation differs  
136 substantially between the *IFNL4* gene and canonical IFNs. Furthermore, we show that  
137 the unique features of the *IFNL4* promoter are evolutionarily conserved.

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## 139 **Results**

140 **Expression of *IFNL4* mRNA is negligible upon viral infection in different human**  
141 **cell types.** The expression of most IFNs is rapidly induced following a viral infection.

142 Upon infection of human A549 cells with Sendai virus (SeV), expression of *IFNL1*  
143 mRNA increased more than 100,000-fold within 5 - 6 hours before it appeared to  
144 reach a plateau (Fig. 1A). The expression of *IFNL4* mRNA also increased  
145 significantly within the first 5 - 6 hours of infection but far less than that of *IFNL1*. At  
146 8 hours after infection, the expression level of *IFNL4* appeared to reach a plateau and  
147 was 300-fold lower than for *IFNL1*. To further investigate the rather low expression  
148 level of *IFNL4* mRNA, we compared the expression of this gene as well as *IFNL1* and  
149 *IFNB1* in four different human cell lines with or without viral infection. Based on the  
150 earlier results, we chose to measure mRNA levels at 6 hours after infection or mock-  
151 infection. As expected, infection with SeV led to a robust expression of *IFNB1* and  
152 *IFNL1* mRNA in A549, THP-1 and PC-3 cells and a moderate expression of *IFNL1*  
153 but not *IFNB1* in HepG2 cells (Fig. 1B). In contrast, the expression of *IFNL4* was  
154 much lower than that of the two canonical IFNs and even after viral infection,  
155 expression of *IFNL4* rarely exceeded the baseline expression of *IFNB1* and *IFNL1*.  
156 With the exception of the HepG2 cells, the absolute expression of *IFNB1* and *IFNL1*  
157 was a 1000-fold higher than that of *IFNL4* following viral infection. Of note, in both  
158 A549 and HepG2 cells, the *IFNL1* and *IFNL4* mRNA levels were close to the  
159 detection limit in the absence of viral infection, and for several of the replicates, no  
160 product was detected within 40 cycles and those measuring points were thus omitted  
161 (Fig. 1B). Cell lines sometimes exhibit minor or major defects in innate immune  
162 pathways and therefore we tested the expression of *IFNL4* mRNA in primary human  
163 airway epithelial cell (hAEC) cultures stimulated with poly(I:C) and compared it to  
164 that of *IFNB1* and *IFNL1* mRNAs (Fig. 1B). In these cells, poly(I:C) stimulation led  
165 to a robust expression of *IFNL1* mRNA whereas *IFNB1* mRNA levels were relatively  
166 high even in the absence of poly(I:C) and did not increase further after poly(I:C)

167 treatment. In contrast, *IFNL4* mRNA levels were below the detection limit both with  
168 and without poly(I:C) stimulation.

169 The overall low expression of *IFNL4* mRNA was surprising to us because a  
170 substantial expression of the *IFNL4* gene was previously reported to occur in  
171 epithelial cells infected by human metapneumovirus (hMPV) (29). Therefore, we  
172 repeated this experiment where we measured induction of *IFNLs* transcripts in A549  
173 cells infected by an influenza A virus (IAV) variant lacking its NS1 gene (IAV  $\Delta$ NS1),  
174 or by hMPV. In contrast to previously published data, hMPV infection did not lead to  
175 any substantial expression of *IFNL4* mRNA in our experiments but did induce the  
176 expression of *IFNL1* mRNA (Fig. 1C). As expected, infection with IAV  $\Delta$ NS1  
177 resulted in a strong induction of *IFNL1* mRNA but only a minor induction of *IFNL4*  
178 mRNA. Altogether, *IFNL4* expression is negligible compared to that of *IFNL1* in  
179 A549 cells after hMPV or IAV  $\Delta$ NS1 infection (Fig. 1C). This leads us to suggest that  
180 *IFNL4* is a non-canonical IFN as it lacks the otherwise defining characteristic of IFNs,  
181 i.e. their strong induction upon viral infection.

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183 **The *IFNL1* but not the *IFNL4* promoter is activated by viral infection or**  
184 **overexpression of MAVS.** To create a system which allowed us to characterize the  
185 *IFNL4* promoter in detail, we cloned a 2,186 bp fragment of the *IFNL1* promoter and  
186 a 2,387 bp fragment of the *IFNL4* promoter in front of a firefly luciferase gene (Fig.  
187 2A). Because IFN regulatory factor 3 (IRF3) is a crucial transcription factor  
188 governing expression of canonical IFNs, we used two ways of activating IRF3:  
189 overexpression of the adaptor protein MAVS, which signals upstream of IRF3, or  
190 infection with SeV. First, HEK293T cells were transfected with either the *IFNL1* or  
191 *IFNL4* promoter reporter construct along with increasing amounts of a construct



192 encoding MAVS (Fig. 2B). The results show that the *IFNL1* promoter is potently  
193 induced by MAVS overexpression whereas this is not the case for the *IFNL4*  
194 promoter. Even at the highest amount of MAVS-encoding construct used, the *IFNL1*  
195 promoter gives an approximately 230-fold stronger luciferase activity than the *IFNL4*  
196 promoter. Next, we repeated the experiment using SeV infection instead of  
197 overexpression of MAVS, with the similar result that the *IFNL1* but not the *IFNL4*  
198 promoter was potently induced by SeV infection (Fig. 2C). This is consistent with the  
199 previous results showing a very low *IFNL4* mRNA expression level in human cell  
200 lines.

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202 **The *IFNL1* but not the *IFNL4* promoter is activated by IRF3 and IRF7 following**  
203 **SeV infection.** The transcription factors IRF3 and IRF7 both play an important role in  
204 controlling expression of canonical IFNs. However, they are member of a larger  
205 family consisting of nine members, IRF1-9. It is possible that activation of the *IFNL4*  
206 promoter requires other members of the IRF family than those needed for expression  
207 of the canonical IFNs. Therefore, we transfected expression constructs encoding the  
208 different IRF members into IRF3 knock out HEK293T cells together with either the  
209 *IFNL4* or the *IFNL1* promoter reporter construct and then infected the cells with SeV  
210 before measuring luciferase activity. Overexpression of both IRF3 and IRF7 led to a  
211 small, yet significant induction of the *IFNL4* promoter upon virus stimulation.  
212 However, this induction is negligible compared to that of the *IFNL1* promoter (Fig.  
213 2D) and underlines the unique regulatory requirement of the *IFNL4* promoter. In  
214 contrast, the *IFNL1* promoter was induced by both IRF3 and IRF7 as expected (Fig.  
215 2E).

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217 **Is the behavior of the *IFNL4* promoter evolutionarily conserved?**

218 The above experiments showed that the human *IFNL4* promoter is functionally  
219 different from the human *IFNL1* promoter. However, since there has been a selection  
220 against a functional *IFNL4* gene in humans (SNP  $\Delta G/TT$ , rs368234815), it is possible  
221 that low *IFNL4* promoter activity is a result of an evolutionary pressure to reduce  
222 *IFNL4* expression. If this is the case, the low activity of the *IFNL4* promoter should  
223 be specific to humans as the selection against an active form of the *IFNL4* gene  
224 ( $\Delta G/TT$ , rs368234815) is a recent event in human evolution (14). To investigate this,  
225 we tested the expression of *IFNL4* mRNA in pigs as well as the activity of *IFNL4*  
226 promoters from several mammalian species. We used primary porcine airway  
227 epithelial cell cultures stimulated with poly(I:C) and measured *IFNL2* and *IFNL4*  
228 mRNA levels by semi-quantitative PCR (Fig. 3). The expression of the porcine *IFNL2*  
229 gene is clearly induced by poly(I:C) after 30 cycles whereas *IFNL4* specific primers  
230 only yielded a faint band after 40 cycles, indicating a rather low expression of *IFNL4*  
231 following poly(I:C) stimulation. This suggests that the difference in expression of  
232 *IFNL4* compared to that observed for canonical IFNs is not unique to humans and  
233 accordingly seems not to be the result of the recent selection against a functional  
234 *IFNL4* gene in humans.

235 This observation prompted us to investigate the activity of the *IFNL4* promoter from a  
236 number of mammalian species. The leucine rich repeat and fibronectin type III  
237 domain containing 1 (*LRFN1*) and syncollin (*SYCN*) genes, which flank each side of  
238 the type III IFN loci, are evolutionarily conserved among mammals (Fig. 4A). We  
239 used those genes to mark the borders of the type III IFN loci and then analyzed the  
240 genomic loci in a number of mammalian species to identify *IFNL4* orthologues. We  
241 analyzed the genomic loci from human, African green monkey, sheep, pig and the

242 house mouse because in these species the type III IFN loci are fully sequenced. The  
243 *IFNL1* gene is present in humans and African green monkey but is absent in sheep,  
244 mouse, and pig, whereas the *IFNL2* and/or *IFNL3* genes can be found in all five  
245 species (Fig. 4A). Many mammals seem to have two highly similar *IFNL4* genes, but  
246 in humans, one of these *IFNL4* genes has become a pseudogene whereas mice have  
247 no *IFNL4* genes. As for sheep and pigs, sheep possess two *IFNL4* genes like many  
248 other ungulates while pigs only possess one *IFNL4* gene. Thus, humans and pigs have  
249 a single *IFNL4* gene while African green monkeys and sheep have two *IFNL4* genes.  
250 We performed an evolutionary analysis of the *IFNL4* genes we identified and  
251 concluded that independent duplications of the *IFNL4* gene must have occurred  
252 several times during mammalian evolution. This makes it difficult to precisely  
253 distinguish between true paralogues and orthologues genes and we therefore chose  
254 those *IFNL4* genes which had the same orientation as the human *IFNL4* gene for our  
255 investigation.

256 To describe if the functionality of the *IFNL4* promoter is evolutionary conserved, we  
257 cloned the *IFNL4* promoters from African green monkey, sheep and pig and added  
258 them to our comparison. As a control, we also cloned the *IFNL2* or *IFNL3* promoter  
259 from these species, except from African green monkey where it was not possible due  
260 to technical limitations. To compare the different *IFNL4* promoters, HEK293T cells  
261 were transfected with the different type III IFN promoter reporter constructs along  
262 with a construct encoding MAVS (Fig. 4B). Our comparison showed that the *IFNL4*  
263 promoter is induced to a much lower degree by overexpression of MAVS than the  
264 *IFNL1/IFNL2/IFNL3* promoters in all four species that we have tested here. The same  
265 results are also seen when we stimulated cells with SeV infection instead of MAVS  
266 overexpression (Fig. 4C). One concern by using non-human promoters in HEK293T

267 cells is the compatibility of those promoters with the human system. However, we  
268 consistently saw strong induction of the *IFNL1/IFNL2/IFNL3* genes and furthermore  
269 the data from the primary pig airway epithelial cells was in agreement with the data  
270 obtained using the pig promoters in the HEK293T cells. Altogether, the results  
271 suggest that the behavior of the *IFNL4* promoter appears to be conserved among  
272 mammals.

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274 **The *IFNL4* promoter is highly conserved and forms a separate evolutionary**  
275 **clade.** The evolutionarily conserved behavior of the *IFNL4* promoter prompted us to  
276 examine the degree of sequence conservation within the *IFNL4* promoter region.  
277 Figure 5A shows a nucleotide alignment of the first 600 base pairs (bp) of the *IFNL4*  
278 promoters, counting from the translational start site, from those species examined in  
279 the previous promoter activity assay. We chose the translational start site to anchor  
280 this alignment for two reasons: *i*) it is clearly defined for all species and *ii*) regulatory  
281 elements can be found both upstream and downstream of the transcriptional start site.  
282 The analysis demonstrated a high degree of conservation suggesting that there has  
283 been a significant selective pressure on this region throughout mammalian evolution.  
284 Next, we calculated an evolutionary tree from a set of *IFNL4* and *IFNL1* promoter  
285 sequences. The promoter sequences form two clearly separated clades according to  
286 which genes they belong to, confirming our previous conclusion that the *IFNL4*  
287 promoter is both evolutionary and functional distinct from the canonical IFN  
288 promoters (here represented by the *IFNL1* promoter) (Fig. 5B). We also calculated a  
289 tree based upon the protein sequences of IFN- $\lambda$ 1 and IFN- $\lambda$ 4 from the same set of  
290 species, and as previously observed (3), the IFN- $\lambda$ 4 sequences form a separate and  
291 distinct clade (Fig. 5C).

292 **The basic *IFNL4* promoter is functional and can be activated by an enhancer**  
293 **element present in the *IFNL1* promoter.** A promoter region can, somewhat  
294 simplified, be described as consisting of a core promoter where the RNA polymerase  
295 II complex assembles, and a series of upstream and/or downstream regulatory  
296 elements. To test if the core promoter of *IFNL4* is functional, we constructed chimera  
297 A combining 100 bp of proximal *IFNL4* promoter and upstream 1,989 bp of *IFNL1*  
298 promoter (Fig 6A). Chimera A is active upon overexpression of MAVS, whereas the  
299 inverse chimera B with the *IFNL1* core promoter fused to the upstream regulatory  
300 elements of the *IFNL4* promoter was largely inactive, indicating that the *IFNL4* core  
301 promoter can be activated by enhancer elements present in the *IFNL1* promoter. To  
302 determine if the IRF binding site of the *IFNL1* promoter functions as an enhancer in  
303 the context of the *IFNL4* promoter, we constructed chimera C. In chimera C, the IRF  
304 binding motif from the *IFNL1* promoter was inserted into the *IFNL4* promoter in the  
305 same position as it occupies in *IFNL1* promoter, which is 100 bp upstream of the  
306 transcription start site (TSS) (Fig 6B). Chimera C is active whereas chimera C with a  
307 mutated IRF site (mutIRF) is inactive (the IRF binding site was mutated by changing  
308 nucleotides CAGTTTC of this motif into AAGCAGA). Thus, by inserting a  
309 functional IRF binding site into context of the *IFNL4* promoter, the promoter becomes  
310 inducible by viral infection. These results confirm that the *IFNL4* promoter is a  
311 potentially functional core promoter sequence.

312  
313 **A non-functional and out of place IRF binding site is found within the *IFNL4***  
314 **promoter.** Above, we demonstrated that insertion of the IRF site from the *IFNL1*  
315 promoter into the *IFNL4* promoter resulted in a virus-inducible activation of the  
316 *IFNL4* promoter. However, one putative IRF site exists within the *IFNL4* promoter.

317 Replacing the canonical IRF site found in the *IFNL1* promoter with the putative IRF  
318 binding site from the *IFNL4* promoter resulted in chimera D (Fig. 6C). Chimera D  
319 exhibited only minimal activity upon MAVS overexpression implying that the IRF  
320 binding site of *IFNL4* is not functional within the context of the *IFNL1* promoter. Not  
321 only does the sequence of the IRF binding sites differ between the *IFNL1* and *IFNL4*  
322 promoters but their positions differ as well. While the IRF binding site in the *IFNL1*  
323 promoter is located relatively close to the TSS (100 bp from the TSS), the IRF  
324 binding site in the *IFNL4* promoter is located further upstream (224 bp from the TSS).  
325 This is more distant to the TSS compared to most canonical IFN promoters. In  
326 chimera E, we inserted the IRF motif of the *IFNL1* promoter into the position of the  
327 putative IRF binding site already found within the *IFNL4* promoter. Thus, chimera C  
328 and E differ only by the position of the inserted IRF binding site, yet only chimera C  
329 is activated by MAVS overexpression, which shows that the position of the IRF  
330 binding site does matter (Fig. 6C). In conclusion, whereas the *IFNL4* promoter  
331 contains a putative IRF binding site this seems to be non-functional.

332

333 **The *IFNL4* promoter contains functional NF- $\kappa$ B sites.** Efficient induction of IFN  
334 normally requires collaboration between the transcription factors IRF3 and NF- $\kappa$ B  
335 and we therefore searched for NF- $\kappa$ B binding sites at the proximal end of the *IFNL4*  
336 promoter. Two such sites were identified. To test if these sites potentially could be  
337 involved in conferring transcriptional activity, we mutated them individually or  
338 together in context of the transcriptionally active chimera C (Fig. 6D). Both mutNF-  
339  $\kappa$ B1 and mutNF- $\kappa$ B1/2 have reduced transcription whereas mutNF- $\kappa$ B2 has a minimal  
340 effect (Fig. 6D). This indicates that the NF- $\kappa$ B1 site is required for transcriptional  
341 activity of chimera C, whereas the NF- $\kappa$ B2 site is less important.

342

343 **Both IRF3 and RNA polymerase II are recruited to the *IFNL4* promoter in**  
344 **response to viral infection.** To investigate if the IRF3 transcription factor and RNA  
345 polymerase II are recruited to the promoter of *IFNL1* and *IFNL4*, we performed  
346 chromatin immune precipitation (ChIP) assays on A549 cells infected by SeV. For  
347 this purpose, we used antibodies against IRF3 and RNA polymerase II as well as IgG  
348 as a control (Fig. 7A-C). The data show that IRF3 is recruited to the promoter region  
349 of both *IFNL1* and *IFNL4* but with a tendency towards lower enrichment of IRF3 on  
350 the *IFNL4* promoter region after virus infection as compared to *IFNL1* (Fig. 7A).  
351 Moreover, we found that RNA polymerase II occupies both promoters after SeV  
352 infection but more RNA polymerase II was detected at the *IFNL1* promoter (Fig. 7B).  
353 Thus, decreased IRF3 and RNA polymerase II recruitment can account for at least  
354 some of the low response to viral infection exhibited by the *IFNL4* promoter as  
355 compared to the *IFNL1* promoter.

356

### 357 Discussion

358 Genetic data has attributed unique properties to the *IFNL4* gene. It protects against  
359 liver fibrosis (17, 19) and hence it is assumed to help dampening or controlling  
360 inflammation in both HCV infected patients and patients with non-alcoholic steatosis  
361 (NASH) (15). Furthermore, its ablation facilitates both spontaneous and treatment-  
362 induced HCV clearance (12). These observations are counterintuitive when taking  
363 into account that IFNs are normally both antiviral and pro-inflammatory and suggest  
364 that the *IFNL4* gene is functionally distinct from the canonical IFNs. We have  
365 conducted a series of experiments to biochemically characterize the IFN- $\lambda$ 4 protein,  
366 but found that the biochemical properties of the IFN- $\lambda$ 4 protein are highly similar to

367 those of other members of the IFN- $\lambda$  family, i.e. the IFN- $\lambda$ 4 protein signals through  
368 the same receptor and induces a set of genes highly similar to that induced by the  
369 IFN- $\lambda$ 3 protein (20, 21).

370 A defining characteristic of IFNs is their ability to be induced by viral infection  
371 through the transcription factors IRF3 or IRF7 (30). Here we demonstrate that while  
372 the *IFNL4* gene has a putative IRF3/7 binding site, this site is either non-functional or  
373 functions very poorly resulting in little or no transcription of the *IFNL4* gene in  
374 response to viral infections. This agrees well with previous data showing very low  
375 levels of *IFNL4* mRNA in the liver of HCV infected patients (25) but contradicts  
376 other findings claiming that *IFNL4* mRNA expression is induced by viral infection *in*  
377 *vitro* (29, 31).

378 A previously published study showed that hMPV infection led to a strong induction  
379 (approximately 40,000-fold) of *IFNL4* mRNA expression in A549 cells when  
380 compared to non-infected cells (29). However, when we tested *IFNL4* gene  
381 expression in hMPV infected A549 cells, we found that the *IFNL4* expression was  
382 weak and much lower than *IFNL1* expression under the same conditions. A different  
383 study showed induction of the *IFNL4* mRNA, measured as fold induction, in SeV  
384 infected PC-3 cells (31). We measured *IFNL4* mRNA levels in PC-3 cells under  
385 similar conditions and although there was an induction of the *IFNL4* mRNA in  
386 infected versus non-infected cells, the expression level was low and comparable to the  
387 level of *IFNL1* mRNA found prior to viral infection. During a virus infection, large  
388 amounts of canonical IFNs are produced and in that context the rather marginal  
389 *IFNL4* expression upon viral infection is unlikely to have significant role. Hence, we  
390 do not believe that the low level of *IFNL4* mRNA produced by PC-3 or A549 cells is  
391 of physiological relevance.



392 We performed a series of assays on different *IFNL4/IFNL1* promoter chimeras using a  
393 luciferase reporter system in HEK293 cells. Those data clearly show that inserting a  
394 functional IRF3 site at the proper position renders the *IFNL4* promoter virus-inducible.  
395 We speculate that the *IFNL4* promoter is regulated by yet unknown stimuli, and the  
396 evolutionary conservation of both the sequence of the *IFNL4* promoter region as well  
397 as its functional characteristics supports this. Our efforts to identify such a stimulus  
398 has so far been in vain, but our preliminary data suggest that neither ER stress, LPS  
399 nor activation of the inflammasome leads to activation of the *IFNL4* gene.

400 Other examples of non-canonical regulation of IFN genes exist. The *IFNE* gene, in  
401 contrast to the other type I IFN genes, is not induced by viral infection but is  
402 specifically expressed in the female reproductive tract where it protects against  
403 infection. Furthermore, the expression of the *IFNE* gene is regulated by estrogen (32).  
404 To sum up, we conclude that the regulation of the *IFNL4* gene is a conserved feature  
405 among mammals and that the *IFNL4* gene is a non-canonical member of the type III  
406 IFN family as it is regulated in a unique way that differs from that of the canonical  
407 IFNs.

## 409 **Materials and methods**

### 410 **Cells**

411 Cell lines used in this study were PC-3 (prostate cancer cell line), A549 (human lung  
412 epithelial cells), HepG2 (liver hepatocellular carcinoma), THP-1 (human monocytic  
413 cells) and IRF3 knock out HEK293T cells (human embryonic kidney cells). PC-3  
414 cells were cultured in F12K medium supplemented with 2 mM L-glutamine, 10%  
415 fetal bovine serum (FBS), 100 U/ml penicillin and 100 µg/ml streptomycin. THP-1  
416 cells were cultured in the RPMI-1640 medium supplemented with 10% FBS, 100

417 U/ml penicillin and 100 µg/ml streptomycin. All other cell lines were cultured in  
418 Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% FBS, 100  
419 U/ml penicillin and 100 µg/ml streptomycin.

420 Well-differentiated human airway epithelial cell cultures from three biological donors  
421 were isolated, established and maintained as previously described (33). Primary  
422 porcine tracheobronchial airway epithelial cells were isolated from post-mortem  
423 material obtained from SPF-pigs. Isolation of cells was performed with protease and  
424 DNase digestion and primary porcine tracheobronchial cells were cultured as  
425 previously described (33) but with a few modifications. For cellular differentiation,  
426 the human epidermal growth factor concentration was increased ten-fold in the air-  
427 liquid interface medium, whereas retinoic acid was two-fold more concentrated. The  
428 epithelial layer was allowed to differentiate for at least four weeks prior to stimulation  
429 experiments.

430

#### 431 **Plasmids**

432 The different promoter sequences used in this study were cloned from genomic DNA  
433 using standard cloning techniques. The sources were THP-1 cells for the human  
434 *IFNL1* and *IFNL4* promoters, Vero cells for the African green monkey *IFNL4*  
435 promoter, Texel sheep peripheral blood mononuclear cells for the sheep *IFNL3* and  
436 *IFNL4* and Göttingen minipig tissue for the pig *IFNL2* and *IFNL4* promoters. Because  
437 the transcriptional start site has not been experimentally verified for most of these  
438 genes, we chose to always include the 5' UTR in the cloned sequence. The sequences  
439 were cloned into the multiple cloning site of the pGL3.1-Basic plasmid (Promega)  
440 and afterwards the remaining sequence between the inserted promoter sequence and  
441 the translational start site of the firefly luciferase gene was deleted by site-directed

442 mutagenesis. The different chimeras and mutants of the human *IFNL1* and *IFNL4*  
443 promoters were constructed using standard cloning techniques and site-directed  
444 mutagenesis. In chimera A, nucleotides -1 to -100 of the *IFNL1* promoter were  
445 replaced by nucleotides -1 to -100 of the *IFNL4* promoter. In chimera A, nucleotides -  
446 1 to -100 of the *IFNL4* promoter were replaced by nucleotides -1 to -98 of the *IFNL1*  
447 promoter. In chimera C, nucleotides -101 to -132 of the *IFNL4* promoter were  
448 replaced with -101 to -134 of the *IFNL1* promoter. In chimera C (mutIRF),  
449 nucleotides -129 to -123 from the *IFNL1* promoter in chimera were changed from  
450 CAGTTTC to AAGCAGA. In chimera D, nucleotides -117 to -132 of the *IFNL1*  
451 promoter were replaced with nucleotides -225 to -235 of the *IFNL4* promoter. In  
452 chimera E, nucleotides -225 to -235 in the *IFNL4* promoter were replaced with  
453 nucleotides -117 to -132 of the *IFNL1* promoter. In chimera C (mutNF- $\kappa$ B1),  
454 nucleotides -69 to -66 of the *IFNL4* promoter in chimera C was changed from ACCC  
455 to CCCT. In chimera C (mutNF- $\kappa$ B2), nucleotides 32 to 35 of the *IFNL4* promoter in  
456 chimera C was changed from CCCA to GGGT. Chimera (mutNF- $\kappa$ B1/2) is a  
457 combination of the two previous chimeras.

458 The plasmids used for expressing IRF2, -4 and -8 (pEF-IRF2, pSV-LS-IRF4 and  
459 pICSBP) were kind gifts from professor Takashi Fujita (Kyoto University, Japan)  
460 whereas the plasmids for expression of IRF3 and MAVS (pcDNA3-IRF3 #32713 and  
461 pEF-BOS-MAVS #27224) were from Addgene. The plasmids used for expressing  
462 IRF1, -5, -6 and -7 were constructed in our laboratory. The sequences of all plasmids  
463 used in this study were verified by Sanger sequencing (GATC Biotech) and detailed  
464 information about them is available upon request.

465

#### 466 **Infections and stimulations**

467 For qPCR assays, cells were seeded in 6-well tissue culture plates at a density of  
468  $6 \times 10^5$  per well. For the THP-1 cells, phorbol 12-myristate 13-acetate (PMA) was  
469 added to a final concentration of 100 nM to trigger differentiation into macrophages.  
470 After resting for 24 hours, the cells were infected with 40 HAU SeV (Cantell strain)  
471 per well for 6 hours. Infection of A549 cells with hMPV was performed as previously  
472 described (29).

473 For luciferase assays, cells were infected 24 hours post transfection with 20 HAU SeV  
474 (Cantell strain) per well for 24 hours.

475 For ChIP assays, cells were seeded in 150 mm tissue culture dishes at a density of  $1 \times$   
476  $10^7$  cells per dish. After resting for 24 hours, the cells were infected with 560 HAU  
477 SeV (Cantell strain) per dish for 4 hours.

478 For qPCR and semi-qPCR, human or porcine airway epithelial cells were treated with  
479 10  $\mu$ g/ml poly(I:C) via the basolateral surface for a duration of 18 hours prior to cell  
480 lysis and total RNA extraction.

481

#### 482 **Quantitative real-time and semi-quantitative PCR**

483 Total RNA was extracted with the E.Z.N.A. Total RNA Kit I (Omega Bio Tek)  
484 according to the manufacturer's instructions. The cDNA synthesis was performed  
485 with 0.5  $\mu$ g RNA using RevertAid Reverse Transcriptase and random hexamer primer  
486 according to the manufacturer's instructions (ThermoFisher Scientific). The cDNA  
487 was quantified by qPCR using SYBR Green I (Roche) and a LightCycler 480  
488 Instrument II (Roche). The following primers were used: human *IFNB1*, forward  
489 ACGCCGCATTGACCATCTAT and reverse GTCTCATTCCAGCCAGTGCT;  
490 human *IFNL1*, forward TTCCAAGCCCACCACAACTG and reverse  
491 GTGACTCTTCCAAGGCGTCC, human *IFNL4*, forward

492 CGGCCTGCCTTGAGCTG and reverse GGGTTTGTGACGCCTCTTCT; human  
493 *HPRT1*, forward CCCTGGCGTCGTGATTAGTG and reverse  
494 CACCCTTTCCAAATCCTCAGC. The cycling parameters were 95°C for 10 min  
495 followed by 40 cycles of 95°C for 10 s, 60°C for 5 s and 72 °C for 4 s. The crossing  
496 points of the amplification curves were determined using the second derivative  
497 method on the LightCycler 480 Instrument II software 1.5 (Roche). The  
498 hypoxanthine-guanine phosphoribosyltransferase (*HPRT1*) gene was used as a  
499 reference gene. The level of mRNA was normalized against internal HPRT mRNA  
500 content. Relative mRNA levels of each target gene were calculated using the  
501 following formula:  $2^{-(Ct(\text{target})-Ct(\text{control}))}$ .

502

503

#### 504 **Semi-quantitative PCR**

505 The following primers were used: human *IFNL1*, forward  
506 GGAAGCAGTTGCGATTTAGCC and reverse GACTCTTCCAAGGCGTCCCT;  
507 human *IFNL4*, forward TTGGCTTCCCTGACGTCTCT and reverse  
508 CTCTTCCTCGTAGCGGTCCC; pig *IFNL2*, forward  
509 GTCCCTCTTGGAGGACTGGA and reverse CTGAGCTGGGACACAGGC; pig  
510 *IFNL4*, forward GATGTCCGTCGCCTCTTGTA and reverse  
511 GCGTCTCTTCCTCATAGTGGT. The PCR was performed as described above for  
512 qPCR and run for 20, 30, or 40 cycles. The PCR products were run on a 1% agarose  
513 TBE gel with a GeneRuler 100 bp Plus DNA Ladder (ThermoFisher Scientific)

514

#### 515 **Transfections**

516 For transfection, cells were seeded in 12-well tissue culture plates at a density of

517  $4 \times 10^5$  cells per well. After resting for 24 hours, and then transfected 24 hours later  
518 using polyethylenimine (PEI). For all transfections, a total of 2  $\mu$ g plasmid was gently  
519 mixed with 6  $\mu$ g PEI in a total volume of 200  $\mu$ l and incubated 15 minutes at room  
520 temperature before adding it drop wise to the cells. The 2  $\mu$ g plasmid always included  
521 50 ng plasmid constitutively expressing *Renilla* luciferase and 1,000 ng pGL3.1  
522 plasmid containing a type III IFN promoter. Unless otherwise stated, 400 ng plasmid  
523 expressing one of the IRFs or MAVS was included in those experiments that required  
524 expression of these proteins. To reach the desired total of 2  $\mu$ g plasmid for each  
525 transfection, an empty pcDNA3.1 plasmid was added accordingly.

526

#### 527 **Luciferase assays**

528 At 24 hours after transfection/infection, cells were lysed with Passive Lysis Buffer  
529 (Promega) and firefly and *Renilla* luciferase activity in the lysate was then measured  
530 using the Dual-Luciferase Reporter Assay System (Promega) according to the  
531 manufacturer's instructions.

532

#### 533 **Chromatin immunoprecipitation (ChIP)**

534 ChIP was performed as previously described (34). The antibodies used were Mouse  
535 IgG Isotype Control (ThermoFisher Scientific), IRF-3 (D83B9) Rabbit mAb (Cell  
536 Signaling), Mouse Anti-RNA polymerase II CTD repeat YSPTSPS antibody [8WG16]  
537 (abcam) and Rabbit Anti-Histone H3 antibody (abcam). The co-immunoprecipitated  
538 DNA was quantified by qPCR as described above except that the cDNA synthesis  
539 step was omitted. The following primers were used: human *IFNL1*, forward  
540 TGAGGCCAGTTGGCTGAAAG and reverse GGAGCCTGATGAGGGAACAG;  
541 human *IFNL4*, forward TCAACACTACACAAGGGCTGG and reverse

542 CGGTTTCCAAATTGTCTCTGTCC; *GAPDH*, forward  
543 GCGTGTAAGGGTCCCCGTCCT, and reverse GTTCAACTGGGCACGCACCGA

544

545

#### 546 **Alignments and phylogenetic trees**

547 All the sequences used for alignments and phylogenetic trees were extracted from the  
548 corresponding genomic reference sequences from NCBI. The accession numbers of  
549 these are NC000019 (human), NC023647 (African green monkey), NC010448  
550 (domesticated pig), NC019471 (domesticated sheep), NW007907093 (polar bear) and  
551 NW006804147 (western European hedgehog). Sequences were aligned using  
552 ClustalW and phylogenetic trees were generated using the Neighbor-Joining method  
553 in MEGA7.

554

#### 555 **Statistical analysis**

556 Statistical analysis was performed in GraphPad Prism 8.2.

557

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566

567 **Author contributions**

568 HZ, MM, ET-D, KGW, NHH, JV-N, LL, RD and HHG designed, performed and  
569 analyzed experiments. RD, ALN, HHG and RH supervised the research. HZ, ET-D,  
570 HHG and RH conceived the project and prepared the manuscript. All authors  
571 commented on the manuscript.

572

573 **Conflict of interest**

574 The authors declare that they have no conflict of interest

575

576 **Figure Legends**

577 **Figure 1. Expression of the *IFNL4* gene is not virus-inducible.** (A) A549 (an  
578 adenocarcinomic alveolar basal epithelial cell line) cells were infected with SeV and  
579 the expression levels of *IFNL4* and *IFNL1* genes were quantified by RT-qPCR at the  
580 indicated time points. Data were calculated relative to internal expression of *HPRT*.  
581 The experiment was performed in biological triplicates and data are presented as  
582 scatter plot with mean  $\pm$  SD (n=3). (B) A549, HepG2 (a hepatocellular carcinoma cell  
583 line), macrophage-like differentiated THP-1 (a monocyte-like cell line before  
584 differentiation), and PC-3 (a prostate cancer cell line) cells were mock-infected or  
585 infected with SeV for 6 hours while human airway epithelial cell (hAEC) cultures  
586 were mock-treated or treated with poly(I:C) for 18 hours. Expression levels of *IFNB1*,  
587 *IFNL4* and *IFNL1* genes were quantified by RT-qPCR. Data were calculated relative  
588 to internal expression of *HPRT*. The dashed line indicates the detection limit in those



589 cases where mRNA levels could not be determined for some replicates because they  
590 were too low. The experiment was performed in biological sextuplicates (left panel)  
591 or triplicates (right panel) and data are presented as scatter plot with mean  $\pm$  SD (n=3  
592 or 6). Statistical significance was determined using an unpaired t test. \*,  $0.01 < P <$   
593  $0.05$ ; ns,  $P \geq 0.05$ . (B) A549 cells were mock-infected or infected with hMPV or IAV  
594  $\Delta$ NS1 for 18 hours. Expression levels of *IFNL1* and *IFNL4* mRNA were assessed by  
595 semiquantitative PCR and visualised by agarose gel electrophoresis. The experiment  
596 was performed in biological duplicates.

597

598 **Figure 2. The *IFNL4* promoter is not activated by the same stimuli that readily**  
599 **activate the *IFNL1* promoter. (A)** The promoter regions of the human *IFNL1* and  
600 *IFNL4* genes corresponding to 2,186 and 2,387 bp, respectively, upstream of their  
601 translation start site were inserted in front of the firefly luciferase coding sequence in  
602 the pGL3.1-Basic plasmid. (B) HEK293T cells were co-transfected with pGL3.1  
603 plasmid containing the *IFNL1* or *IFNL4* promoter, a plasmid constitutively expressing  
604 the *Renilla* luciferase gene and increasing amounts of a plasmid expressing MAVS.  
605 At 24 hours post transfection, firefly/*Renilla* luciferase activity was quantified. The  
606 experiment was performed in biological triplicates and the data are presented as bar  
607 chart and scatter plot with mean  $\pm$  SD (n=3). (C) HEK293T cells were co-transfected  
608 with pGL3.1 plasmid containing the *IFNL1* or *IFNL4* promoter and a plasmid  
609 constitutively expressing the *Renilla* luciferase gene. At 24 hours post transfection,  
610 the cells were infected with SeV for another 24 hours before quantifying  
611 firefly/*Renilla* luciferase activity. One representative out of two independent  
612 experiments is shown, each with biological triplicates. The data are presented as bar  
613 chart and scatter plot with mean  $\pm$  SD (n=3). (D-E) IRF3 knock out HEK293T cells

614 were co-transfected with pGL3.1 plasmid containing the *IFNL1* (D) or *IFNL4* (E)  
615 promoter in front of a firefly luciferase gene, a plasmid constitutively expressing the  
616 *Renilla* luciferase gene and a plasmid constitutively expressing IRF1, IRF2, IRF3,  
617 IRF4, IRF5, IRF6, IRF7 or IRF8. At 24 hours post transfection, the cells were  
618 infected with SeV for another 24 hours before quantifying firefly/*Renilla* luciferase  
619 activity. One representative out of two independent experiments is shown, each with  
620 biological triplicates. The data are presented as bar chart and scatter plot with mean  $\pm$   
621 SD (n=3). Statistical significance was determined using an unpaired t test. \*\*\*\*;  $P <$   
622 0.0001, \*\*\*,  $0.0001 < P < 0.001$ ; \*\*,  $0.001 < P < 0.01$ ; \*,  $0.01 < P < 0.05$ ; ns,  $P \geq$   
623 0.05.

624

625 **Figure 3. The *IFNL4* gene is poorly expressed in primary porcine epithelial cells.**

626 Porcine airway epithelial cells (pAECs) were treated with 10  $\mu$ g/ml poly(I:C) via the  
627 basolateral surface for 18 hours. Expression levels of *IFNL2* and *IFNL4* mRNA were  
628 assessed by semiquantitative PCR and visualised by agarose gel electrophoresis. The  
629 experiment was performed in biological triplicates.

630

631 **Figure 4. The weak functionality of the *IFNL4* promoter is evolutionary  
632 conserved among mammals. (A) Overview of the type III IFN loci in human,**

633 African green monkey, sheep, mouse, and pig. The type III IFN genes illustrated by  
634 different colors share a common synteny in mammals and are flanked on each side by  
635 the leucine rich repeat and fibronectin type III domain containing 1 (*LRFN1*) and  
636 syncollin (*SYCN*) genes. Black arrows indicate the direction of transcription for each  
637 gene. (B) HEK293T cells were co-transfected with pGL3.1 plasmid containing the

638 *IFNL4* or *IFNL1/2/3* promoter from human, African green monkey, pig or sheep, a  
639 plasmid constitutively expressing the *Renilla* luciferase gene and a plasmid  
640 constitutively expressing MAVS. At 24 hours post transfection, firefly/*Renilla*  
641 luciferase activity was quantified. One representative out of two independent  
642 experiments is shown, each with biological triplicates. The data are presented as  
643 scatter plot with mean  $\pm$  SD (n=3). (C) HEK293T cells were co-transfected with  
644 pGL3.1 plasmid containing the *IFNL4* or *IFNL1/2/3* promoter from human, African  
645 green monkey, pig and sheep and a plasmid constitutively expressing the *Renilla*  
646 luciferase gene. At 24 hours post transfection, the cells were infected with SeV for  
647 another 24 hours before quantifying firefly/*Renilla* luciferase activity. One  
648 representative out of two independent experiments is shown, each with biological  
649 triplicates. The data are presented as scatter plot with mean  $\pm$  SD (n=3). Statistical  
650 significance was determined using an unpaired t test. \*\*\*\*\*,  $P < 0.0001$ , \*\*\*,  $0.0001 <$   
651  $P < 0.001$ ; \*\*,  $0.001 < P < 0.01$ ; \*,  $0.01 < P < 0.05$ ; ns,  $P \geq 0.05$ .

652

653 **Figure 5. Conservation of the *IFNL4* promoter among mammals.** (A) Alignment  
654 of the proximal/core promoter and the 5' UTR of *IFNL4* from human, African green  
655 monkey, pig and sheep. The transcriptional start site (TSS) as well as putative IRF  
656 and NF- $\kappa$ B binding sites are indicated in the human sequence. (B) Phylogenetic tree  
657 of *IFNL1* and *IFNL4* from human (*H. sapiens*), African green monkey (*C. sabaues*),  
658 sheep (*O. aries*), pig (*S. scrofa*), western European hedgehog (*E. europaeus*), polar  
659 bear (*U. maritimus*) based on the sequence of their proximal/core promoter and 5'  
660 UTR. The sequences were aligned using ClustalW and the tree was generated by the  
661 Neighbor-Joining method. (C) Same as in (B) but using the amino acid sequences of  
662 the proteins instead. Both trees are drawn to scale, with branch lengths measured in

663 the number of substitutions per site.

664

665 **Figure 6. Insertion of a functional IRF binding site in the *IFNL4* promoter**  
666 **renders it virus-inducible. (A-D)** HEK293T cells were co-transfected with a pGL3.1  
667 plasmid containing the *IFNL1* or *IFNL4* promoter or chimeras thereof, a plasmid  
668 constitutively expressing the *Renilla* luciferase gene and a plasmid constitutively  
669 expressing MAVS. At 24 hours post transfection, firefly/*Renilla* luciferase activity  
670 was quantified. One representative out of two independent experiments is shown,  
671 each with biological triplicates. The data are presented as scatter plot with mean  $\pm$  SD  
672 (n=3). **(A)** In chimera A and B, the first 100 bp upstream of the TSS has been  
673 swapped between the *IFNL1* and *IFNL4* promoters as indicated by the colors on the  
674 drawing. **(B)** In chimera C, the IRF binding site from *IFNL1* was inserted into the  
675 *IFNL4* promoter at the same relative position it occupied in *IFNL1*. In chimera C  
676 (mutIRF), the *IFNL1* IRF binding site in chimera C was mutated to render it inactive.  
677 **(C)** In chimera D, the IRF binding site in *IFNL1* was replaced with the putative IRF  
678 binding site from *IFNL4*. In chimera E, the putative IRF binding site in *IFNL4* was  
679 replaced with the IRF binding site from *IFNL1*. **(D)** In chimera C (mutNF- $\kappa$ B1), the  
680 NF- $\kappa$ B binding site located upstream of the TSS in *IFNL4* was mutated to render it  
681 inactive. In chimera C (mutNF- $\kappa$ B2), the NF- $\kappa$ B binding site located downstream of  
682 the TSS in *IFNL4* was mutated to render it inactive. In chimera C (mutNF- $\kappa$ B1/2)  
683 both NF- $\kappa$ B binding sites were simultaneous mutated. Statistical significance was  
684 determined using ANOVA and Dunnett's T3 multiple comparison test. \*\*\*, 0.0001 <  
685 P < 0.001; \*\*, 0.001 < P < 0.01; ns, P  $\geq$  0.05.

686

687 **Figure 7. Recruitment of IRF3 and RNA polymerase II to the *IFNL4* and *IFNL1***  
688 **promoters.** A549 cells were mock-infected or infected with SeV for 4 hours before  
689 performing ChIP with antibodies against IRF3 (**A**), RNA polymerase II (**B**) and IgG  
690 as control (**C**). One representative out of two independent experiments is shown, each  
691 with biological duplicates. The data are presented as bar chart and scatter plot with  
692 mean.

693

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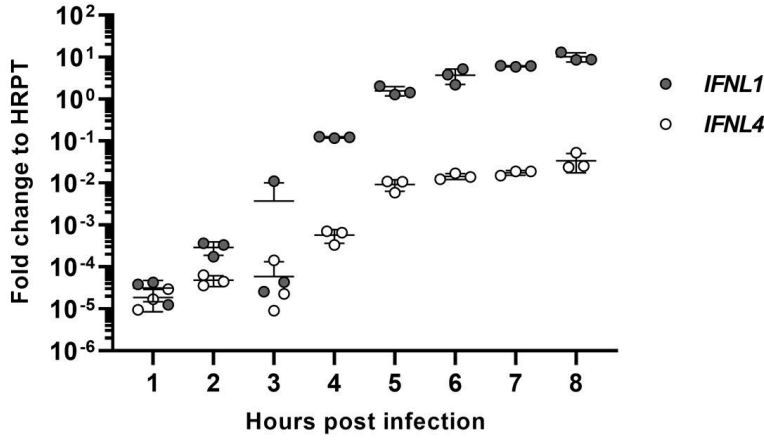
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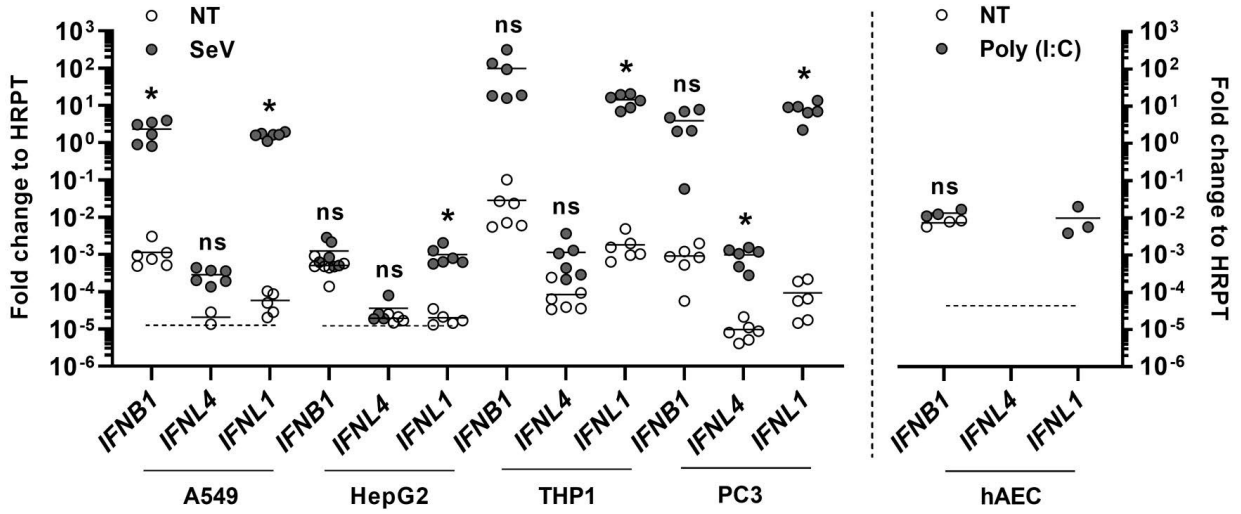
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- 830



**A**



**B**



**C**

